

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffrey E. Russel Examiner #: 62785 Date: 2-3-2005
 Art Unit: 1654 Phone Number: 571-272-0769 Serial Number: 10/001,945
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle) PAPER DISK E-MAIL
REM 3C18 (mailbox), 3D19 (office)

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

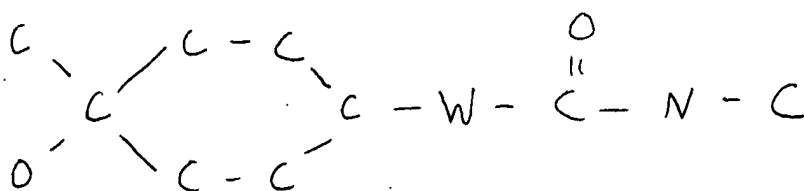
Title of invention: Modulation Of Angiogenesis

Inventors (please provide full names): G. Olson, C. Self, L. Lee, C. Cook, J. Bicktoft, B. Morgan,
C. Arico-Muendel

Earliest Priority Filing Date: 11-1-2001

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search the following partial structure:



where W is O or N.

Thank you.

for

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 12:15:42 ; Search time 163 Seconds
(without alignments)
16.609 Million cell updates/sec

Title: US-10-001-945A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1171057

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		Query		ID	Description
		Match	Length	DB			
1	26	100.0	7	5	AAE26706		Aae26706 Matrix me
2	26	100.0	7	5	AAE26707		Aae26707 Matrix me
3	26	100.0	7	7	ADC33666		Adc33666 Matrix me
4	26	100.0	7	7	ADC33667		Adc33667 Matrix me
5	26	100.0	7	7	AAE39186		Aae39186 Angiogene
6	26	100.0	7	7	AAE39185		Aae39185 Angiogene
7	26	100.0	7	7	ABW02759		Abw02759 Angiogene
8	26	100.0	7	7	ABW02760		Abw02760 Angiogene
9	26	100.0	9	8	ADO39412		Ado39412 Contiguou

10	26	100.0	11	2	AAR25097	Aar25097 bGRF prod
11	26	100.0	12	5	ABB80826	Abb80826 Heparin b
12	26	100.0	12	6	ABR64030	Abr64030 E. coli p
13	26	100.0	12	7	ADC44494	Adc44494 Endotheli
14	26	100.0	13	6	ABU14452	Abu14452 hFSH pept
15	26	100.0	13	6	ABU14453	Abu14453 hFSH pept
16	26	100.0	13	6	ABU14451	Abu14451 hFSH pept
17	26	100.0	13	6	ABU14449	Abu14449 hFSH pept
18	26	100.0	13	6	ABU14448	Abu14448 hFSH pept
19	26	100.0	13	6	ABU14450	Abu14450 hFSH pept
20	26	100.0	15	8	ADS88902	Ads88902 Peptide e
21	26	100.0	17	6	ADA74731	Ada74731 Tryptical
22	26	100.0	18	6	ADA74730	Ada74730 Tryptical
23	26	100.0	19	2	AAW16890	Aaw16890 Helicobac
24	26	100.0	19	6	ADA74729	Ada74729 Tryptical
25	26	100.0	19	8	ADN17105	Adn17105 Second ge
26	26	100.0	20	5	AAU99411	Aau99411 Human ECS
27	26	100.0	20	8	ADO80138	Ado80138 Human mag
28	26	100.0	20	8	ADS51924	Ads51924 tRNA (gua
29	26	100.0	22	4	AAO01366	Aao01366 Human pol
30	26	100.0	24	4	AAO04347	Aao04347 Human pol
31	26	100.0	26	4	AAO12271	Aao12271 Human pol
32	26	100.0	26	4	AAO05706	Aao05706 Human pol
33	26	100.0	27	4	AAO11884	Aao11884 Human pol
34	26	100.0	29	4	AAO05109	Aao05109 Human pol
35	26	100.0	30	4	AAB64810	Aab64810 Human sec
36	26	100.0	30	4	AAO04013	Aao04013 Human pol
37	26	100.0	30	4	AAO03914	Aao03914 Human pol
38	26	100.0	30	4	AAO04497	Aao04497 Human pol
39	26	100.0	31	4	AAO05488	Aao05488 Human pol
40	26	100.0	31	4	AAO10805	Aao10805 Human pol
41	26	100.0	31	4	AAO13369	Aao13369 Human pol
42	26	100.0	31	4	AAO05850	Aao05850 Human pol
43	26	100.0	32	4	AAO11531	Aao11531 Human pol
44	26	100.0	32	4	AAO11435	Aao11435 Human pol
45	26	100.0	32	4	AAO05724	Aao05724 Human pol

ALIGNMENTS

RESULT 1

AAE26706

ID AAE26706 standard; peptide; 7 AA.

XX

AC AAE26706;

XX

DT 13-DEC-2002 (first entry)

XX

DE Matrix metalloprotease (MMP) substrate peptide #15.

XX

KW Angiogenesis; methionine aminopeptidase; MetAP-2; matrix metalloprotease;
KW MMP; therapy; autoimmune disease; rheumatoid arthritis; ocular disorder;
KW diabetic retinopathy; skin disorder; paediatric disorder; angiofibroma;
KW psoriasis; cancer; sarcoma; carcinoma; hypertrophic scar.

XX

OS Unidentified.

XX
 FH Key Location/Qualifiers
 FT Modified-site 2
 FT /note= "L-cyclohexylalanine"
 FT Modified-site 4
 FT /note= "L-2-aminobutyric acid"
 FT Modified-site 5
 FT /note= "Methyl cysteine; This residue is shown as Xaa in
 FT the sequence shown as SEQ ID NO: 16 in the sequence
 FT listing of the specification"
 XX
 PN WO200242295-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 01-NOV-2001; 2001WO-US046086.
 XX
 PR 01-NOV-2000; 2000US-00704251.
 PR 05-OCT-2001; 2001US-00972772.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Olson GL, Self C, Lee L, Cook CM, Birktoft J;
 XX
 DR WPI; 2002-666821/71.
 XX
 PT New compounds comprising MetAP-2 inhibitory core e.g. 1-
 PT oxaspiro(2.5)octane derivative, coupled to peptide which is matrix
 PT metalloprotease substrate, useful for treating e.g. cancer or rheumatoid
 PT arthritis, are angiogenesis inhibitors.
 XX
 PS Claim 47; Page 77; 98pp; English.
 XX
 CC The present invention relates to novel angiogenesis inhibitor compounds
 CC comprising a methionine aminopeptidase (MetAP-2) inhibitory core (e.g. 1-
 CC oxaspiro (2.5) octane derivative), coupled to a peptide which is a matrix
 CC metalloprotease (MMP) substrate. Compounds of the invention are useful
 CC for treating angiogenic diseases such as autoimmune diseases (e.g.
 CC cancer, rheumatoid arthritis). They are also useful for treating ocular
 CC disorders (e.g. diabetic retinopathy), disorders affecting the skin (e.g.
 CC psoriasis), cancer (e.g. carcinoma, sarcoma), paediatric disorders (e.g.
 CC angiofibroma) and disorders associated with surgery (e.g. hypertrophic
 CC scars). The present sequence is MMP substrate peptide
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 26; DB 5; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
 ||||:||
 Db 1 PXAXCHA 7

ADO39412

ID ADO39412 standard; peptide; 9 AA.

XX

AC ADO39412;

XX

DT 29-JUL-2004 (first entry)

XX

DE Contiguous capillary-related horse apomyoglobin peptide SeqID12.

XX

KW contiguous capillary; electrically conductive; pores; analyte;

KW electrolyte; electrospray source; electrophoresis separation;

KW electrical conductivity; macromolecular analyte detection sensitivity;

KW CE-ESI-MS device; horse.

XX

OS Equus caballus.

XX

PN WO2004038752-A2.

XX

PD 06-MAY-2004.

XX

PF 20-OCT-2003; 2003WO-US033200.

XX

PR 21-OCT-2002; 2002US-0420003P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Janini G, Isaaq HJ, Veenstra TD, Conrads TP, Wilkens KL;

XX

DR WPI; 2004-390013/36.

XX

PT Contiguous capillary useful for separating and electrospraying a fluid

PT e.g. peptides and proteins includes inlet end, spray tip and an

PT electrically conductive portion in proximity to the spray tip to block

PT the passage of analyte through it.

XX

PS Example; SEQ ID NO 12; 53pp; English.

XX

CC This invention relates to a novel contiguous capillary which includes an
CC inlet to supply fluid into the capillary, a spray tip for spraying fluid
CC out of the capillary and an electrically conductive portion in proximity
CC to the spray tip. The electrically conductive portion has pores of size
CC that block the passage of analyte and permits the passage of electrolyte
CC through it. The capillary is useful as an electrospray source in the
CC electrophoresis separation and electrospraying of fluid containing
CC analyte and electrolyte, for example peptides and proteins. The invention
CC minimises analyte loss while maintaining electrical conductivity and does
CC not require a sheathed opening or break in the capillary near the spray
CC tip. The capillaries are rugged, simple in design and effect an increase
CC in macromolecular analyte detection sensitivity of up to about 100-fold
CC in CE-ESI-MS devices. The invention enables the high-resolution
CC identification of analytes. The present sequence is that of a horse
CC apomyoglobin tryptic digest peptide which was used in the exemplification
CC of the invention.

XX

SQ Sequence 9 AA;

Query Match

100.0%; Score 26; DB 8; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|::||
Db 1 PLAQSHA 7

RESULT 10

AAR25097

ID AAR25097 standard; protein; 11 AA.

XX

AC AAR25097;

XX

DT 25-MAR-2003 (revised)

DT 23-DEC-1992 (first entry)

XX

DE bGRF prodrug analogue 16.

XX

KW Bovine growth hormone releasing factor; dipeptidylpeptidase IV; DPP IV;
KW purification; medicament.

XX

OS Synthetic.

XX

PN WO9210576-A1.

XX

PD 25-JUN-1992.

XX

PF 12-DEC-1991; 91WO-US009152.

XX

PR 13-DEC-1990; 90US-00626727.

XX

PA (UPJO) UPJOHN CO.

XX

PI Kubiak TM, Sharma SK;

XX

DR WPI; 1992-234631/28.

XX

PT Non-naturally occurring fusion protein prodrug - is cleaved in-vivo by
PT host di:peptidyl peptides IV to achieve sustained release, e.g. of growth
PT hormone.

XX

PS Disclosure; Page 38; 55pp; English.

XX

CC The sequences given in AAR25082-109 and AAR25247-62 are N-terminally
CC extended bovine growth hormone releasing factor (bGRF) prodrug analogues.
CC The N-terminal extension is cleavable by dipeptidylpeptidase IV (DPP IV).
CC Exposure of these bGRF prodrug analogues to DPP IV results in their
CC conversion to desirable proteins. These prodrugs are converted to
CC prodrugs using a patients endogenous DPP IV, thereby achieving sustained
CC presence of the active drug in a patient and reducing the frequency of
CC administration. These proteins are useful in purification methods were
CC the N-terminal extension facilitates purification. They may also be used
CC to prepare a medicament. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|::||
Db 3 PHAHAHA 9

Search completed: February 11, 2005, 12:34:39
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 12:28:57 ; Search time 43 Seconds
(without alignments)
12.152 Million cell updates/sec

Title: US-10-001-945A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 324380

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8
Result Query
No. Score Match Length DB ID Description

1	26	100.0	7	4	US-09-704-251-16	Sequence 16, Appl
2	26	100.0	7	4	US-09-704-251-17	Sequence 17, Appl
3	26	100.0	11	1	US-08-211-942-18	Sequence 18, Appl
4	26	100.0	11	5	PCT-US91-09152-16	Sequence 16, Appl
5	26	100.0	19	1	US-08-211-942-1	Sequence 1, Appli
6	26	100.0	26	3	US-08-974-549A-57	Sequence 57, Appl
7	26	100.0	26	4	US-08-912-951-57	Sequence 57, Appl
8	26	100.0	26	4	US-09-402-181B-57	Sequence 57, Appl
9	26	100.0	26	4	US-09-721-456-57	Sequence 57, Appl
10	26	100.0	37	1	US-08-340-428B-7	Sequence 7, Appli
11	26	100.0	37	5	PCT-US93-07306-7	Sequence 7, Appli
12	26	100.0	50	4	US-09-621-976-5211	Sequence 5211, Ap
13	26	100.0	53	4	US-09-621-976-6427	Sequence 6427, Ap
14	26	100.0	54	4	US-09-513-999C-4567	Sequence 4567, Ap
15	26	100.0	59	4	US-09-621-976-4384	Sequence 4384, Ap
16	26	100.0	60	3	US-08-817-787-22	Sequence 22, Appl
17	26	100.0	60	4	US-09-621-976-6245	Sequence 6245, Ap
18	26	100.0	60	4	US-09-583-808-22	Sequence 22, Appl
19	26	100.0	61	4	US-09-252-991A-29862	Sequence 29862, A
20	26	100.0	63	4	US-09-621-976-7548	Sequence 7548, Ap
21	26	100.0	66	4	US-09-270-767-40087	Sequence 40087, A
22	26	100.0	66	4	US-09-270-767-55303	Sequence 55303, A
23	26	100.0	67	4	US-09-252-991A-26524	Sequence 26524, A
24	26	100.0	67	4	US-09-489-039A-12320	Sequence 12320, A
25	26	100.0	72	4	US-09-621-976-4512	Sequence 4512, Ap
26	26	100.0	74	4	US-09-270-767-60432	Sequence 60432, A
27	26	100.0	80	4	US-09-205-258-939	Sequence 939, App
28	26	100.0	80	4	US-09-621-976-5334	Sequence 5334, Ap
29	26	100.0	86	3	US-09-134-001C-5488	Sequence 5488, Ap
30	26	100.0	88	4	US-09-489-039A-8981	Sequence 8981, Ap
31	26	100.0	89	4	US-09-621-976-6766	Sequence 6766, Ap
32	26	100.0	94	4	US-09-328-352-5643	Sequence 5643, Ap
33	26	100.0	98	4	US-09-543-681A-6937	Sequence 6937, Ap
34	23	88.5	11	3	US-08-893-526A-16	Sequence 16, Appl
35	23	88.5	16	2	US-08-528-057-12	Sequence 12, Appl
36	23	88.5	19	4	US-09-132-769-12	Sequence 12, Appl
37	23	88.5	22	4	US-09-464-152A-17	Sequence 17, Appl
38	23	88.5	29	4	US-09-513-783A-132	Sequence 132, App
39	23	88.5	29	4	US-09-430-656-132	Sequence 132, App
40	23	88.5	52	4	US-09-270-767-36792	Sequence 36792, A
41	23	88.5	52	4	US-09-270-767-52009	Sequence 52009, A
42	23	88.5	58	4	US-09-270-767-37591	Sequence 37591, A
43	23	88.5	58	4	US-09-270-767-52808	Sequence 52808, A
44	23	88.5	64	4	US-09-270-767-40507	Sequence 40507, A
45	23	88.5	64	4	US-09-270-767-55723	Sequence 55723, A

ALIGNMENTS

RESULT 1

US-09-704-251-16

; Sequence 16, Application US/09704251

; Patent No. 6548477

; GENERAL INFORMATION:

; APPLICANT: Olson, Gary L.

; APPLICANT: Self, Christopher


```

; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106
; CURRENT APPLICATION NUMBER: US/09/704,251
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; OTHER INFORMATION: Xaa at position 2 represents L-cyclohexylalanine
; OTHER INFORMATION: Xaa at position 4 represents L-a-aminobutyryl
; OTHER INFORMATION: Xaa at position 5 represents methylated cysteine
US-09-704-251-16

```

```

Query Match          100.0%; Score 26; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 PXAXXHA 7
        |||||
Db      1 PXAXXHA 7

```

RESULT 3

US-08-211-942-18

; Sequence 18, Application US/08211942

; Patent No. 5523287

; GENERAL INFORMATION:

; APPLICANT: Friedrich, Thomas

; APPLICANT: Bialojan, Siegfried

; APPLICANT: Kroeger, Burkhard

; APPLICANT: Kuenast, Christoph

; TITLE OF INVENTION: No. 5523287el thrombin-inhibitory protein from assassin

; TITLE OF INVENTION: bugs.

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Keil & Weinkauff

; STREET: 1101 Connecticut Avenue

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage

; COMPUTER: IBM AT-compatible, 80486 processor

; OPERATING SYSTEM: MS-DOS version 6.0

; SOFTWARE: WordPerfect version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/211,942

; FILING DATE:

; CLASSIFICATION: 435
; CLASSIFICATION: C07K 13/00
; CLASSIFICATION: A61K 37/64
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP92/02450
; FILING DATE: 27-OCT-1992
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-211-942-18

Query Match 100.0%; Score 26; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 36;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|::||
Db 5 PCACPHA 11

Search completed: February 11, 2005, 12:39:05
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 12:37:43 ; Search time 129 Seconds
(without alignments)
17.731 Million cell updates/sec

Title: US-10-001-945A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 585885

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

```

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	26	100.0	7	9	US-09-972-772-16	Sequence 16, Appl
2	26	100.0	7	9	US-09-972-772-17	Sequence 17, Appl
3	26	100.0	7	13	US-10-001-945-16	Sequence 16, Appl
4	26	100.0	7	13	US-10-001-945-17	Sequence 17, Appl
5	26	100.0	7	14	US-10-138-935-16	Sequence 16, Appl
6	26	100.0	7	14	US-10-138-935-17	Sequence 17, Appl
7	26	100.0	12	14	US-10-286-457-222	Sequence 222, App
8	26	100.0	13	16	US-10-203-969A-513	Sequence 513, App
9	26	100.0	13	16	US-10-203-969A-514	Sequence 514, App
10	26	100.0	13	16	US-10-203-969A-515	Sequence 515, App
11	26	100.0	13	16	US-10-203-969A-516	Sequence 516, App
12	26	100.0	13	16	US-10-203-969A-517	Sequence 517, App
13	26	100.0	13	16	US-10-203-969A-518	Sequence 518, App
14	26	100.0	13	16	US-10-642-553-361	Sequence 361, App
15	26	100.0	13	16	US-10-642-553-362	Sequence 362, App
16	26	100.0	13	16	US-10-642-553-363	Sequence 363, App
17	26	100.0	13	16	US-10-642-553-364	Sequence 364, App
18	26	100.0	13	16	US-10-642-553-365	Sequence 365, App
19	26	100.0	13	16	US-10-642-553-366	Sequence 366, App
20	26	100.0	17	15	US-10-289-009-14	Sequence 14, Appl
21	26	100.0	18	15	US-10-289-009-13	Sequence 13, Appl
22	26	100.0	19	15	US-10-289-009-12	Sequence 12, Appl
23	26	100.0	20	15	US-10-430-685-80	Sequence 80, Appl
24	26	100.0	20	15	US-10-416-090-2	Sequence 2, Appli
25	26	100.0	26	14	US-10-044-692-57	Sequence 57, Appl
26	26	100.0	26	14	US-10-044-539-57	Sequence 57, Appl
27	26	100.0	26	15	US-10-325-810-57	Sequence 57, Appl
28	26	100.0	26	17	US-10-877-146-57	Sequence 57, Appl
29	26	100.0	33	14	US-10-029-386-31686	Sequence 31686, A

30	26	100.0	37	14	US-10-164-279-51	Sequence 51, Appl
31	26	100.0	37	16	US-10-437-963-178440	Sequence 178440,
32	26	100.0	38	11	US-09-833-245-614	Sequence 614, App
33	26	100.0	38	15	US-10-424-599-265177	Sequence 265177,
34	26	100.0	40	9	US-09-764-869-880	Sequence 880, App
35	26	100.0	40	14	US-10-091-504-880	Sequence 880, App
36	26	100.0	40	15	US-10-227-577-880	Sequence 880, App
37	26	100.0	42	15	US-10-424-599-211724	Sequence 211724,
38	26	100.0	43	16	US-10-437-963-133265	Sequence 133265,
39	26	100.0	45	16	US-10-475-446-28	Sequence 28, Appl
40	26	100.0	46	9	US-09-764-869-854	Sequence 854, App
41	26	100.0	46	14	US-10-091-504-854	Sequence 854, App
42	26	100.0	46	15	US-10-227-577-854	Sequence 854, App
43	26	100.0	47	9	US-09-864-761-42772	Sequence 42772, A
44	26	100.0	48	14	US-10-144-929-168	Sequence 168, App
45	26	100.0	48	14	US-10-029-386-28596	Sequence 28596, A

ALIGNMENTS

RESULT 1

US-09-972-772-16

```
; Sequence 16, Application US/09972772
; Publication No. US20020193298A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106CP
; CURRENT APPLICATION NUMBER: US/09/972,772
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; NAME/KEY: VARIANT
; LOCATION: 2
; OTHER INFORMATION: Xaa at position 2 represents L-cyclohexylalanine
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 represents L-a-aminobutyryl
; NAME/KEY: VARIANT
; LOCATION: 5
; OTHER INFORMATION: Xaa at position 5 represents methylated cysteine
US-09-972-772-16
```

Query Match 100.0%; Score 26; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|||||||
Db 1 PXAXXHA 7

RESULT 8

US-10-203-969A-513

; Sequence 513, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hFSH derived
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(13)
US-10-203-969A-513

Query Match 100.0%; Score 26; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|::||
Db 6 PGAAHHA 12

Search completed: February 11, 2005, 12:49:59
Job time : 130 secs

OM protein - protein search, using sw model

Run on: February 11, 2005, 12:28:27 ; Search time 38 Seconds
(without alignments)
17.724 Million cell updates/sec

Title: US-10-001-945A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 37678

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	26	100.0	55	2	C82705	hypothetical prote
2	26	100.0	68	2	I38590	hypothetical prote
3	26	100.0	80	2	F82684	hypothetical prote
4	26	100.0	82	2	T04476	acclimation protei
5	26	100.0	84	2	AH2724	hypothetical prote
6	26	100.0	84	2	D97506	hypothetical prote
7	26	100.0	93	2	S14020	hypothetical prote
8	23	88.5	51	2	T08488	hypothetical prote
9	23	88.5	51	2	T07563	hypothetical prote
10	23	88.5	52	2	C84395	hypothetical prote
11	23	88.5	57	2	AF1381	hypothetical prote
12	23	88.5	62	2	S73032	hypothetical prote
13	23	88.5	64	2	E87083	50S ribosomal prot
14	23	88.5	64	2	E70619	probable ribosomal
15	23	88.5	69	1	B35537	cytochrome-c oxida
16	23	88.5	69	1	OSHU8	cytochrome-c oxida
17	23	88.5	69	2	S71929	cytochrome-c oxida
18	23	88.5	82	1	CCPS5S	cytochrome c551 [v

19	23	88.5	85	2	C82706	hypothetical prote
20	23	88.5	90	2	I38889	transmembrane prot
21	23	88.5	92	2	B75602	hypothetical prote
22	23	88.5	93	2	S14314	neutrophil cationi
23	23	88.5	93	2	S21169	neutrophil cationi
24	23	88.5	95	2	AG0505	probable membrane
25	23	88.5	95	2	D83360	hypothetical prote
26	22	84.6	12	2	S65730	hemoglobin, extrac
27	22	84.6	15	2	S36893	ribosomal protein
28	22	84.6	20	2	S72501	protein kinase C i
29	22	84.6	20	2	PH0110	style glycoprotein
30	22	84.6	21	2	S46550	actin-related prot
31	22	84.6	23	2	D34047	stylar glycoprotei
32	22	84.6	25	2	A58647	alphaA-conotoxin P
33	22	84.6	34	2	E82284	hypothetical prote
34	22	84.6	37	2	S14101	apolipophorin III
35	22	84.6	39	2	D85649	hypothetical prote
36	22	84.6	41	2	S06270	T-cell receptor de
37	22	84.6	42	2	G90911	hypothetical prote
38	22	84.6	46	2	A60495	T-cell receptor be
39	22	84.6	47	2	E81833	hypothetical prote
40	22	84.6	49	2	B24696	tissue kallikrein
41	22	84.6	49	2	T37008	hypothetical prote
42	22	84.6	49	2	B83712	hypothetical prote
43	22	84.6	51	2	E81212	50S ribosomal prot
44	22	84.6	53	2	H84319	hypothetical prote
45	22	84.6	53	2	H82738	hypothetical prote

ALIGNMENTS

RESULT 1

C82705

hypothetical protein XF1238 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: C82705

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: C82705

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-55 <SIM>

A;Cross-references: UNIPROT:Q9PDZ0; GB:AE003958; GB:AE003849; NID:g9106217;

PIDN:AAF84048.1; GSPDB:GN00128; XFSC:XF1238

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros, M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Colauto, N.B.; Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.;

Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.;
Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco,
M.C.; Frohme, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.;
Gomes, S.L.; Gruber, A.; Ho, P.L.; Hoheisel, J.D.; Junqueira, M.L.; Kemper,
E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.;
Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado,
J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques,
M.V.; Martins, E.A.L.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.;
Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento,
A.L.T.O.; Netto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira,
M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto,
B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.;
Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.;
Santelli, R.V.; Sawasaki, H.E.

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da
Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza,
A.P.; Terenzi, M.F.; Truffi, D.; Tsai, S.M.; Tshako, M.H.; Vallada, H.; Van
Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zatz, M.;
Meidanis, J.; Setubal, J.C.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF1238

Query Match 100.0%; Score 26; DB 2; Length 55;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|:|
Db 14 PYAKQHA 20

Search completed: February 11, 2005, 12:38:18
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 12:16:47 ; Search time 167 Seconds
(without alignments)
21.464 Million cell updates/sec

Title: US-10-001-945A-16
Perfect score: 26
Sequence: 1 PXAXXHA 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 259284

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	26	100.0	29	2	Q65HQ6 bacillus li
2	26	100.0	46	2	Q7Z4A7 homo sapien
3	26	100.0	51	2	Q9XST0 canis famil
4	26	100.0	53	2	Q8XY57 ralstonia s
5	26	100.0	54	2	Q68IP5 conus marmo
6	26	100.0	55	2	Q9PDZ0 xylella fas
7	26	100.0	59	2	Q62K88 burkholderi
8	26	100.0	59	2	Q7UUG5 rhodopirell
9	26	100.0	62	2	Q6PN82 conus marmo
10	26	100.0	64	2	Q6PN83 conus marmo
11	26	100.0	66	2	Q6PN84 conus marmo
12	26	100.0	66	2	Q8RYT9 oryza sativ
13	26	100.0	67	2	Q63F35 bacillus ce
14	26	100.0	69	2	Q51084 neisseria m
15	26	100.0	73	2	Q6ZLG6 oryza sativ
16	26	100.0	73	2	Q8FNI9 corynebacte
17	26	100.0	76	2	Q6K7I6 oryza sativ
18	26	100.0	78	2	Q6AFX8 leifsonia x
19	26	100.0	80	2	Q9PDG2 xylella fas
20	26	100.0	81	2	Q84Z16 oryza sativ
21	26	100.0	82	2	Q40033 hordeum vul
22	26	100.0	82	2	Q6SEH3 xenopus lae
23	26	100.0	84	2	Q87MM4 vibrio para
24	26	100.0	84	2	Q8UG39 agrobacteri
25	26	100.0	85	2	Q8S520 cucumis mel
26	26	100.0	85	2	Q8NTQ4 corynebacte
27	26	100.0	86	2	Q71DC3 drosophila
28	26	100.0	87	2	Q8W0D9 oryza sativ
29	26	100.0	87	2	Q9XGU9 orobanche r
30	26	100.0	87	2	Q84EQ2 wautersia o
31	26	100.0	88	2	Q7UGH0 rhodopirell
32	26	100.0	88	2	Q7VZL6 bordetella
33	26	100.0	90	1	NPP3_DROME Q9vv28 drosophila

34	26	100.0	90	2	Q9BGV8	Q9bgv8 macaca fasc
35	26	100.0	91	2	Q6ILY2	Q6ily2 drosophila
36	26	100.0	93	2	Q99198	Q99198 chlamydomon
37	26	100.0	93	2	Q7UWB2	Q7uwb2 rhodopirell
38	26	100.0	93	2	Q82GB4	Q82gb4 streptomyce
39	26	100.0	94	2	Q6IIR6	Q6iir6 drosophila
40	26	100.0	94	2	Q8XW71	Q8xw71 ralstonia s
41	26	100.0	95	2	Q9P0F7	Q9p0f7 homo sapien
42	26	100.0	97	2	Q6ASY5	Q6asy5 oryza sativ
43	26	100.0	97	2	Q6ESH3	Q6esh3 oryza sativ
44	26	100.0	98	2	Q6ABF7	Q6abf7 propionibac
45	26	100.0	99	2	Q8WVH6	Q8wvh6 homo sapien

ALIGNMENTS

RESULT 1

Q65HQ6

ID Q65HQ6 PRELIMINARY; PRT; 29 AA.
AC Q65HQ6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BLi02534;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
DR EMBL; AE017333; AAU41408.1; -.
KW Hypothetical protein.
SQ SEQUENCE 29 AA; 3050 MW; DEE9A2AEE7D3304F CRC64;

Query Match 100.0%; Score 26; DB 2; Length 29;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PXAXXHA 7
|:|:|
Db 8 PTAASHA 14

Search completed: February 11, 2005, 12:37:34
Job time : 170 secs

=> fil reg; d stat que 17
FILE 'REGISTRY' ENTERED AT 17:05:07 ON 14 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 13 FEB 2005 HIGHEST RN 830317-64-1
DICTIONARY FILE UPDATES: 13 FEB 2005 HIGHEST RN 830317-64-1

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

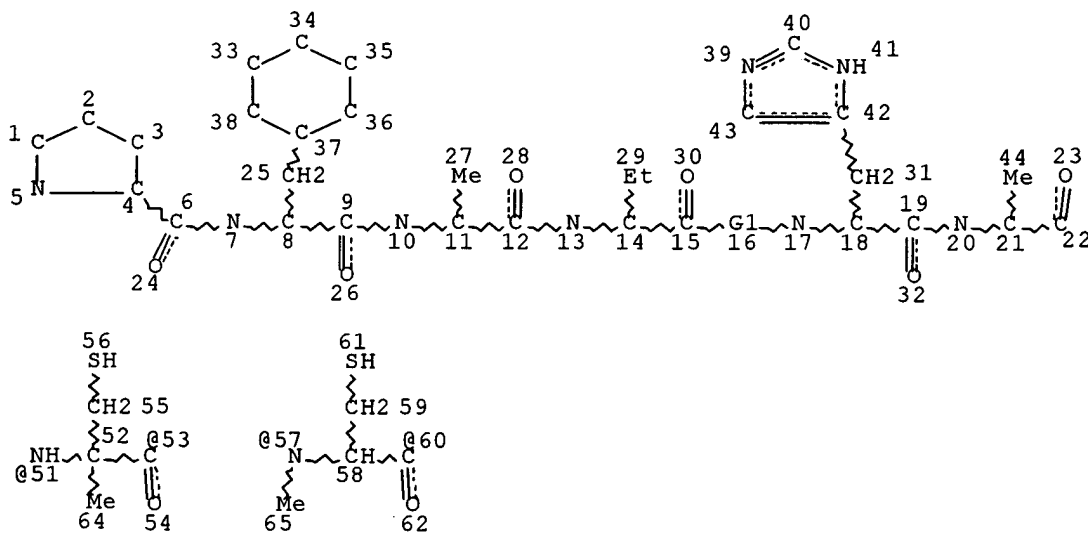
Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

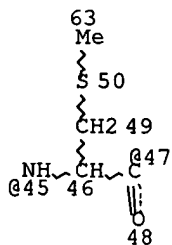
Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

L5

STR



Page 1-A



Page 2-A

VAR G1=51-15 53-17/57-15 60-17/45-15 47-17

NODE ATTRIBUTES:
DEFAULT MLEVEL IS ATOM
DEFAULT ECLEVEL IS LIMITED

GRAPH ATTRIBUTES:
RING(S) ARE ISOLATED OR EMBEDDED
NUMBER OF NODES IS 65

STEREO ATTRIBUTES: NONE
L7 1 SEA FILE=REGISTRY SSS FUL L5

100.0% PROCESSED 1473 ITERATIONS 1 ANSWERS
SEARCH TIME: 00.00.01

=> d sqide l7

L7 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2005 ACS on STN
RN 478412-67-8 REGISTRY
CN L-Alanine, L-prolyl-3-cyclohexyl-L-alanyl-L-alanyl-(2S)-2-aminobutanoyl-S-methyl-L-cysteinyl-L-histidyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 14: PN: US20020193298 SEQID: 16 claimed protein

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 7

NTE modified (modifications unspecified)

type	location		description
uncommon	Abu-4	-	-
modification	Ala-2	-	cyclohexyl<Chx>
modification	Cys-5	-	methyl<Me>

PATENT ANNOTATIONS (PNTE):

Sequence |Patent

Source |Reference

Not Given|US2002193298

|claimed

|SEQID 16

SEQ 1 PAAXCHA

MF C34 H55 N9 O8 S

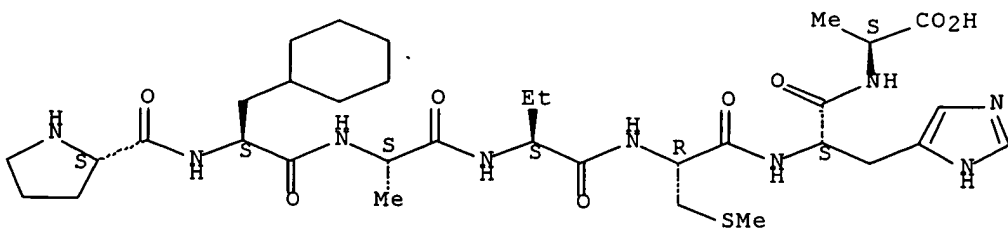
SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

DT.CA CAplus document type: Patent

RL.P Roles from patents: BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

Absolute stereochemistry.



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

2 REFERENCES IN FILE CA (1907 TO DATE)
2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> fil capl uspatf toxcenter; s l7
FILE 'CAPLUS' ENTERED AT 17:05:34 ON 14 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPATFULL' ENTERED AT 17:05:34 ON 14 FEB 2005
CA INDEXING COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'TOXCENTER' ENTERED AT 17:05:34 ON 14 FEB 2005
COPYRIGHT (C) 2005 ACS

L8 6 L7

=> dup rem l8
PROCESSING COMPLETED FOR L8
L9 2 DUP REM L8 (4 DUPLICATES REMOVED)
 ANSWERS '1-2' FROM FILE CAPLUS

=> d ibib ed abs hitrn 1-2; fil hom

L9 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2003:455053 CAPLUS Full-text
DOCUMENT NUMBER: 139:7179
TITLE: Preparation of compounds comprising a methionine
 aminopeptidase 2 (MetAP-2) inhibitory core coupled to
 a peptide for modulation of angiogenesis
INVENTOR(S): Olson, Gary L.; Self, Christopher; Lee, Lily; Cook,
 Charles Michael; Birktoft, Jens; Morgan, Barry;
 Arico-Muendel, Christopher C.
PATENT ASSIGNEE(S): Praecis Pharmaceuticals Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 48 pp., Cont.-in-part of U.S.
 Ser. No. 1,945.
 CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003109671	A1	20030612	US 2002-138935	20020502
US 6548477	B1	20030415	US 2000-704251	20001101
US 2002193298	A1	20021219	US 2001-972772	20011005
US 2002151493	A1	20021017	US 2001-1945	20011101
WO 2003092608	A2	20031113	WO 2003-US13623	20030502
WO 2003092608	A3	20040115		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT,
TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
EP 1503749 A2 20050209 EP 2003-724378 20030502

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
PRIORITY APPLN. INFO.: US 2000-704251 A2 20001101
US 2001-972772 A2 20011005
US 2001-1945 A2 20011101
US 2002-138935 A 20020502
WO 2003-US13623 W 20030502

OTHER SOURCE(S): MARPAT 139:7179

ED Entered STN: 13 Jun 2003

AB The invention provides angiogenesis inhibitor compds. A-W-CONR1-Xn-CR3R4-Z- P [A is a Met-AP-2 inhibitory core; W is O or NR2; R1, R2 are H or alkyl; X is alkylene or substituted alkylene; n is 0 or 1; R3, R4 are H, (un)substituted alkyl or (hetero)aryl; or CR3R4 is carbocyclic, heterocyclic, or alkylene; Z is CO or alkylene-CO and P is a peptide comprising 1 to about 100 amino acid residues attached at its amino terminus to Z or a group OR5 or NR6R7, where R5-R7 are H, alkyl, (un)substituted alkyl or azacycloalkyl or NR6R7 is (un)substituted heterocyclyl; or Z is O, NR6 (R8 = H or alkyl), alkylene-O, or alkylene-NR8 and P is H, alkyl or a peptide consisting of 1 to about 100 amino acid residues attached at its carboxy terminus to Z] comprising a MetAP-2 inhibitory core coupled to a peptide, as well as pharmaceutical compns. comprising the angiogenesis inhibitor compds. Thus, (3R,4S,5S,6R)-5-methoxy-4-[(2R, 3R)-2-methyl-3-(3-methylbut-2-enyl)oxiranyl]-1-oxaspiro[2.5]oct-6-ylcarbonyl-L-valine Me ester, prepared by acylation of L-valine Me ester hydrochloride, showed IC50 = 4.7 nM for inhibition of MetAP-2.

IT 478412-67-8P

RL: PNU (Preparation, unclassified); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

(preparation of peptide MetAP-2 inhibitory core derivs. for modulation of angiogenesis)

L9 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 2002:965105 CAPLUS Full-text

DOCUMENT NUMBER: 138:33374

TITLE: Therapeutic agents and methods of use thereof for the modulation of angiogenesis

INVENTOR(S): Olson, Gary L.; Self, Christopher; Lee, Lily; Cook, Charles Michael; Birktoft, Jens

PATENT ASSIGNEE(S): Praecis Pharmaceuticals Inc., USA

SOURCE: U.S. Pat. Appl. Publ., 38 pp., Cont.-in-part of U. S. Ser. No. 704,251.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 4

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002193298	A1	20021219	US 2001-972772	20011005
US 6548477	B1	20030415	US 2000-704251	20001101
CA 2426703	AA	20020530	CA 2001-2426703	20011101
WO 2002042295	A2	20020530	WO 2001-US46086	20011101
WO 2002042295	A3	20030220		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,

PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA,
 UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
 BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002039479	A5	20020603	AU 2002-39479	20011101
US 2002151493	A1	20021017	US 2001-1945	20011101
EP 1330447	A2	20030730	EP 2001-987241	20011101

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

JP 2004531466	T2	20041014	JP 2002-544429	20011101
US 2003109671	A1	20030612	US 2002-138935	20020502
NO 2003001978	A	20030611	NO 2003-1978	20030430

PRIORITY APPLN. INFO.:

US 2000-704251	A2	20001101
US 2001-972772	A	20011005
US 2001-1945	A2	20011101
WO 2001-US46086	W	20011101

OTHER SOURCE(S): MARPAT 138:33374

ED Entered STN: 20 Dec 2002

AB The present invention provides angiogenesis inhibitor compds. comprising a MetAP-2 (methionine aminopeptidase-2)-inhibitory fumagillin core coupled to a peptide, as well as pharmaceutical compns. comprising the angiogenesis inhibitor compds. and a pharmaceutically acceptable carrier. The present invention also provides methods of treating an angiogenic disease, e.g., cancer, in a subject by administering to the subject a therapeutically effective amount of one or more of the angiogenesis inhibitor compds. of the invention.

IT **478412-67-8P**

RL: PNU (Preparation, unclassified); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)

(MetAP-2-inhibitory peptides for the modulation of angiogenesis)

FILE 'HOME' ENTERED AT 17:05:52 ON 14 FEB 2005

=>